

Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**

x_dropoff: **0** expect: **10.00** wordsize: **3** Filter View option **Standard**

Masking character option **X for protein, n for nucleot** Masking color option **Black**

Show CDS translation

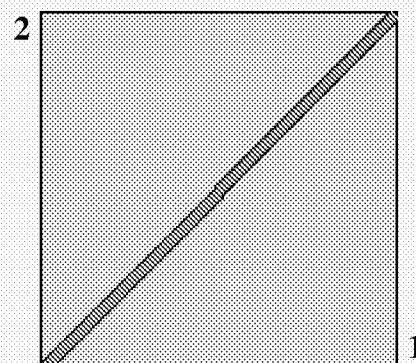
Align

Sequence 1: gi|6706916|spike glycoprotein [bovine coronavirus] Genbank Accession# AAF25499

Length = 1363 (1 .. 1363)

Sequence 2: unnamed protein product SEQ ID NO: 4

Length = 1363 (1 .. 1363)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 2625 bits (6803), Expect = 0.0
 Identities = 1311/1363 (96%), Positives = 1337/1363 (98%), Gaps = 0/1363 (0%)

Query	1	Sequence	Length
Query	1	MFLILLISLPMALAVIGDLKCTTVSINDVDTGVPSVSTDVDTVNGLGTYYVLDRLVYLNT	60
		MFLILLISLPMA AVIGDLKCTTVSINDVDTG PS+STD VDVTNGLGTYYVLDRLVYLNT	
Sbjct	1	MFLILLISLPMAFAVIGDLKCTTVSINDVDTGAPSISTDVVDVTNGLGTYYVLDRLVYLNT	60
Query	61	TLLLNGYYPTSGSTYRNMALKGTLLLSTLWFKPPFLSDFINGIFAKVKNTKVIKNGVMYS	120
		TLLLNGYYPTSGSTYRNMALKGTLLLSTLWFKPPFLSDFI+G+FAVKVKNTKVIK+GV+YS	
Sbjct	61	TLLLNGYYPTSGSTYRNMALKGTLLLSTLWFKPPFLSDFIDGVFAVKVKNTKVIKDGVVYS	120
Query	121	EFPAITIGSTFVNTSYSVVVQPHHTNLDNKLQGLLEISVCQYTMCEYPTICHPNLGNRR	180

Sbjct	121	EFFPAITIGSTFVNNTSYSVVVQPHTTNLDNKLQGLLEISVCQYTM C+YPHT+CHPNLGN+R EFFPAITIGSTFVNNTSYSVVVQPHTTNLDNKLQGLLEISVCQYTMCDYPHTMCHPNLGNKR	180
Query	181	IELWHWDTGVVSCLYKRNFTYDVNADYLYHFYQEGGTFYAYFTDTGVVTKFLFNVYLGT IELWHWDTGVV CLYKRNFTYDVNADYLY HFYQEGGTFYAYFTDTGVVTKFLF+VYLGT	240
Sbjct	181	IELWHWDTGVVPCLYKRNFTYDVNADYLYSHFYQEGGTFYAYFTDTGVVTKFLFHVYLGT	240
Query	241	VLSHYYVMP LTCNSAMTLEYWVTPLTSKQYLLAFNQDGVI FNAVDCKSDFMSEIKCKTLS VLSHYYVMP LTCNSAMTLEYWVTPLT KQYLLAFNQDGVI FNAVDCKSDFMSEIKCKTLS	300
Sbjct	241	VLSHYYVMP LTCNSAMTLEYWVTPLTFKQYLLAFNQDGVI FNAVDCKSDFMSEIKCKTLS	300
Query	301	IAPSTGVYELNGYTVQPIADVYRRIPNL PDCNIEAWLNDKSVPSP LNWERKTF SNCNFNM IAPSTGVYELNGYTVQPIADVYRRIPNL PDCNIEAWLNDKSVPSP LNWERKTF SNCNFNM	360
Sbjct	301	IAPSTGVYELNGYTVQPIADVYRRIPNL PDCNIEAWLNDKSVPSP LNWERKTF SNCNFNM	360
Query	361	SSLMSFIQADSFTCNNIDA AKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRI SSLMSFIQADSFTCNNIDA AKIYGMCF SITIDKFAIPNGRKVDLQ+GNLGYLQSFNYRI	420
Sbjct	361	SSLMSFIQADSFTCNNIDA AKIYGMCFSSITIDKFAIPNGRKVDLQMGNLGYLQSFNYRI	420
Query	421	DTTATSCQLYYNLPAANVSVRFNPSTWNRRFGTEQS VFKPQPVGVFTDHDVVAQHCF DTTATSCQLYYNLPA+NVS+SRFNPS WNRRFGTEQS VFKPQPVGVFTDHDVVAQHCF	480
Sbjct	421	DTTATSCQLYYNLPAANVSVRFNPSTWNRRFGTEQS VFKPQPVGVFTDHDVVAQHCF	480
Query	481	KAPTNFCPC KLDGSLCVGSGSGIDAGYKNSGIGTCPAGTNYL TCHNAAQCNC LCTPDPI KAPTNFCPC KLDGSLCVGSGSGIDAGYKNSGIGTCPAGTNYL TCHNAAQCNC LCTPDPI	540
Sbjct	481	KAPTNFCPC KLDGSLCVGSGFGIDAGYKNSGIGTCPAGTNYL TCHNAAQCNC LCTPDPI	540
Query	541	SKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPQ AFLGWSVDSCLQGDRCNI SKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQP+AFLGWSVDSCLQGDRCNI	600
Sbjct	541	SKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPKAFLGWSVDSCLQGDRCNI	600
Query	601	FANFILHDVNSGTTCSTD LQKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNSWQNL FANFILH VNSGTTCSTD LQKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNSWQNL	660
Sbjct	601	FANFILH VNSGTTCSTD LQKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNSWQNL	660
Query	661	YDSNGNLYGFRDYL TNRTFMIRSCYS GRVSAFHANSSE PALLFRNIK CNYVFNNTLSRQ YDSNGNLYGFRDYL TNRTFMIRSCYS GRVSAFH+NSSE PALLFRNIK CNYVFNNTLSRQ	720
Sbjct	661	YDSNGNLYGFRDYL TNRTFMIRSCYS GRVSAFH+NSSE PALLFRNIK CNYVFNNTLSRQ	720
Query	721	LQPINYFDSYLGCVNADNSTSSAVQTCDLTVGSGYCVDY STKRRSRAIT TGYRFTNFE LQPINYFDSYLGCVNADNSTSS+VQTCDLTVGSGYDY ST+RRSRR ITTGYRFTNFE	780
Sbjct	721	LQPINYFDSYLGCVNADNSTSSVQTCDLTVGSGYWDY STQRRSRR ITTGYRFTNFE	780
Query	781	PFTVNSVND SLEPVGG LYEI QIPSEFTIGNMEEFIQISSPKVTIDCSAFVCGDYAACKSQ PFTVNSVND SLEPVGG LYEI QIPSEFTIGNMEEFIQISSPKVTIDCSAFVCGDYAACKSQ	840
Sbjct	781	PFTVNPVND SLEPVGG LYEI QIPSEFTIGNMEEFIQISSPKVTIDCSAFVCGDYAACKSQ	840
Query	841	LVEYGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDDINFSPVL	900

Sbjct	841	LVEYGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGFNFNVDDINFSPVLS	900
Query	901	GCLGSDCNKVSSRSAIEDLLFSKVQLSDVGFVEAYNNCTGGAEIRDLCVQSYNGIKVLP	960
Sbjct	901	GCLGSECNKVSSRSAIEDLLFSKVQLSDVGFVDAYNNCTGGAEIRDLCVQSYNGIKVLP	960
Query	961	PLLSHQISGYTLAATSASLFPWSAAAGVPFYLNQYRINGIGVTMDVLSQNQKLIANA	1020
Query	961	PLLSHQISGYTLAAT ASLFPPWSAAAGVPFYLNQYRINGIGVTMDV+QNQKLI+NA	1020
Sbjct	961	PLLSHQISGYTLAATFASLFPWSAAAGVPFYLNQYRINGIGVTMDVLTQNQKLIISNA	1020
Query	1021	FNNALDAIQEGFDATNSALVKIQAVVNANAEEALNNLQQLSNRFGAISSSLQEILSRLDA	1080
Sbjct	1021	FNNALDAIQEGFDATNSALVKIQAVVNANAEEALNNLQQLSN+FGAIS+SLQEILSRLDA	1080
Query	1081	LEAQHQIDRLINGRLTALNAYVSQQLSDSTLVFSAAQAMEKVNECVKSQSSRINF CGNG	1140
Sbjct	1081	LEAQHQIDRLINGRLTALNAYVSQQLSDSTLVFSAAQAMEKVNECVKSQSSRINF CGNG	1140
Query	1141	NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVN VNNTWMFT	1200
Sbjct	1141	NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVN VNNTWMFT	1200
Query	1201	GSGYYYPEPITGNVVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPD	1260
Sbjct	1201	GSGYYYPEPITGNVVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPD	1260
Query	1261	LSLDYINVTFQLDQDEMNRQEAIKVLNQSYINLKDITYEYYVKWPWYVWLLIGAGVA	1320
Sbjct	1261	LSLDYINVTFQLDQDEMNRQEAIKVLNHSYINLKDITYEYYVKWPWYVWLLIGAGVA	1320
Query	1321	MLVLLFFICCCTGCGTSCFKCGGCCDDYTGHQELVIKTSHDD	1363
Sbjct	1321	MLVLLFFICCCTGCGTSCFKCGGCCDDYTGHQELVIKTSHDD	1363

CPU time: 0.05 user secs. 0.03 sys. secs. 0.08 total secs.